

10/574084

SEQUENCE LISTING

IAP5 Rec'd PCT/PTO 30 MAR 2006

<110> ENKAM Pharmaceuticals A/S

<120> A method of modulating cell survival, differentiation and/or synaptic plasticity

<130> P 810 PC00

<160> 45

<170> PatentIn version 3.1

<210> 1

<211> 13

<212> PRT

<213> Artificial sequence

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<223> rat NCAM Ig1 fragment: amino acid residues 35-47

<400> 1

Trp Phe Ser Pro Asn Gly Glu Lys Leu Ser Pro Asn Gln
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<210> 2

<211> 14

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<223> rat NCAM Ig1 fragment: amino acid residues 75-88

<400> 2

Tyr Lys Cys Val Val Thr Ala Glu Asp Gly Thr Gln Ser Glu
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<211> 12

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<223> rat NCAM Ig3 fragment: amino acid residues 213-224

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Thr Leu Val Ala Asp Ala Asp Gly Phe Pro Glu Pro
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<210> 4

<211> 9

<212> PRT

<213> Artificial sequence

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<223> rat NCAM Ig2 fragment: amino acid residues 156-164

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Gln Ile Arg Gly Ile Lys Lys Thr Asp
1 5

<210> 5

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<223> rat NCAM Ig2 fragment: amino acid residues 144-146

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Asp Val Arg
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<212> PRT

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<223> rat NCAM Ig2 fragment: amino acid residues 158-164

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Arg Gly Ile Lys Lys Thr Asp
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<210> 7

<211> 10

<212> PRT

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<223> rat NCAM Ig2 fragment: amino acid residues 144-146 and 158-164

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Asp Val Arg Arg Gly Ile Lys Lys Thr Asp
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<210> 8

<211> 5

<212> PRT

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<223> rat NCAM Ig2 fragment: amino acid residues 111-115

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Lys Glu Gly Glu Asp
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<210> 9

<211> 8

<212> PRT

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<220>

<223> rat NCAM Ig2 fragment: amino acid residues 157-164

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Ile Arg Gly Ile Lys Lys Thr Asp
1 5

<210> 10

<211> 14

<212> PRT

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<223> rat NCAM Ig2 fragment: amino acid residues 111-115 and 157-164

<400> 10

Lys Glu Gly Glu Asp Gly Ile Arg Gly Ile Lys Lys Thr Asp
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<210> 11

<211> 5

<212> PRT

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<223> rat NCAM Ig3 fragment: amino acid residues 260-264

<400> 11

Asp Lys Asn Asp Glu
1 5

<210> 12

<211> 12

<212> PRT

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<223> rat NCAM Ig3 fragment: amino acid residues 194-205

<400> 12

Thr Val Gln Ala Arg Asn Ser Ile Val Asn Ala Thr
1 5 10

<210> 13

<211> 9

<212> PRT

<213> Artificial sequence

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<223> rat NCAM Ig3 fragment: amino acid residues 281-289

<400> 13

Ser Ile His Leu Lys Val Phe Ala Lys
1 5

<210> 14

<211> 9

<212> PRT

<213> Artificial sequence

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<223> rat NCAM Ig2 fragment: amino acid residues 150-158

<400> 14

Leu Ser Asn Asn Tyr Leu Gln Ile Arg
1 5

<210> 15

<211> 12

<212> PRT

<213> Artificial sequence

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<223> rat NCAM Ig2 fragment: amino acid residues 146-157

<400> 15

Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile
1 5 10

<210> 16

<211> 16

<212> PRT

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<223> rat NCAM Ig2 fragment: amino acid residues 142-157

<400> 16

Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile
1 5 10 15

<210> 17

<211> 12

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<223> rat NCAM Ig2 fragment: amino acid residues 108-119

<400> 17

Gln Glu Phe Lys Glu Gly Glu Asp Ala Val Ile Val
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<210> 18

<211> 11

<212> PRT

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<223> rat NCAM Ig2 fragment: amino acid residues 111-121

<400> 18

Lys Glu Gly Glu Asp Ala Val Ile Val Cys Asp
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<210> 19

<211> 12

<212> PRT

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<223> rat NCAM Ig1 fragment: amino acid residues 10-21

<400> 19

Gly Glu Ile Ser Val Gly Glu Ser Lys Phe Phe Leu
1 5 10

<210> 20

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 243-263

<400> 20

Lys	His	Ile	Phe	Ser	Asp	Asp	Ser	Ser	Glu	Leu	Thr	Ile	Arg	Asn	Val
1				5				10					15		

Asp	Lys	Asn	Asp	Glu
	20			

<210> 21

<211> 12

<212> PRT

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<223> rat NCAM Ig1fragment : amino acid residues 10-21 containing mutation F19A

<400> 21

Gly	Glu	Ile	Ser	Val	Gly	Glu	Ser	Lys	Ala	Phe	Leu
1				5				10			

<210> 22

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAN Ig1 fragment: amino acid residues 10-21 containing mutations F19A and F20A

<400> 22

Gly	Glu	Ile	Ser	Val	Gly	Glu	Ser	Lys	Ala	Ala	Leu
1				5				10			

<210> 23

<211> 21

<212> PRT

<213> Artificial sequence

<220>

<223> chicken NCAM Ig3 fragment: amino acid residues 243-263

<400> 23

Lys Tyr Ser Phe Asn Tyr Asp Gly Ser Glu Leu Ile Ile Lys Lys Val
1 5 10 15

Asp Lys Ser Asp Glu
20

<210> 24

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 244-253

<400> 24

Lys His Ile Phe Ser Asp Asp Ser Ser Glu
1 5 10

<210> 25

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> chicken NCAM Ig3 fragment: amino acid residues 243-252

<400> 25

Lys Tyr Ser Phe Asn Tyr Asp Gly Ser Glu
1 5 10

<210> 26

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 281-289 containing mutations K285A and F287S

<400> 26

Ser Ile His Leu Ala Val Ala Ala Lys
1 5

<210> 27

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig3 fragment: amino acid residues 281-289 containing mutations K285A and F287G

<400> 27

Ser Ile His Leu Ala Val Gly Ala Lys
1 5

<210> 28

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> rat NCAM Ig2 fragment: amino acid residues 172-182

<400> 28

Gly Arg Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys
1 5 10

<210> 29

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> upper PCR primer

<400> 29

tctctcgaga actgcaggta gatattgtt

29

<210> 30

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> lower PCR primer

<400> 30

aaacccgggt tactttgcaa agacctt

27

<210> 31

<211> 25

<212> DNA

<213> Artificial sequence

<220>

<223> upper PCR primer

<400> 31

gaatacgtaa ctgtccaggc cagac

<210> 32

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> lower PCR primer

<400> 32

aaaccttaggt tactttgcaa agacctt

27

<210> 33

<211> 75

<212> DNA

<213> Artificial sequence

<220>

<223> upper PCR primer

<400> 33

ctgcaggtag atattgtcc cagccaagga gccatcagcg ttggagcctc cgccttcttc

60

ctgtgtcaag tggca

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<210> 34

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> upper PCR primer

<400> 34

ggcgacagtt cggcgtaac catcaggaat gtggac

36

<210> 35
<211> 39
<212> DNA
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<400> 35
ggtaacgcc gaactgtcgc cactgaagat gtgcttctc 39

<210> 36
<211> 45
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<400> 36
aaaccttaggt tactttgctg cgactgcgag gtggatggag gcatac 45

<210> 37
<211> 29
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<400> 37
tctctcgagt tctgcaggta gatattgtt 29

<210> 38
<211> 36
<212> DNA

<213> Artificial sequence

<220>

<223> PCR primer

<400> 38

aaataacgtaa ctgtccaggc cgccccagagc atcgtg

36

<210> 39

<211> 16

<212> PRT

<213> Artificial sequence

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<223> rat NCAM Ig2 fragment: amino acid residues 133-148

<400> 39

Lys His Lys Gly Arg Asp Val Ile Leu Lys Lys Asp Val Arg Phe Ile
1 5 10 15

<210> 40

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> NCAM Ig1 fargment: CD-strands

<400> 40

Ala Phe Ser Pro Asn Gly Glu Lys Leu Ser Pro Asn Gln
1 5 10

<210> 41

<211> 14

<212> PRT

<213> Artificial sequence

<220>

<223> NCAM Ig1 fragment: FG-strands

<400> 41

Ala Lys Ser Val Val Thr Ala Glu Asp Gly Thr Gln Ser Glu
1 5 10

<210> 42

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> NCAM Ig2 fragment: CD-strands

<400> 42

Asp Val Arg Arg Gly Ile Lys Lys Thr Asp
1 5 10

<210> 43

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> NCAM Ig2 fragment: EF-strands

<400> 43

Gln Ile Arg Gly Ile Lys Lys Thr Asp
1 5

<210> 44

<211> 858

<212> PRT

<213> Rattus norvegicus

<400> 44

Met Leu Arg Thr Lys Asp Leu Ile Trp Thr Leu Phe Phe Leu Gly Thr
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Ala Val Ser Leu Gln Val Asp Ile Val Pro Ser Gln Gly Glu Ile Ser
20 25 30

Val Gly Glu Ser Lys Phe Phe Leu Cys Gln Val Ala Gly Asp Ala Lys
35 40 45

Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Ser Pro
50 55 60

Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Asp Asp Ser Ser Thr
65 70 75 80

Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys
85 90 95

Val Val Thr Ala Glu Asp Gly Thr Gln Ser Glu Ala Thr Val Asn Val
100 105 110

Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu
115 120 125

Phe Lys Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser
130 135 140

Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu
145 150 155 160

Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile
165 170 175

Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg
180 185 190

Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val
195 200 205

Asn Val Pro Pro Thr Val Gln Ala Arg Gln Ser Ile Val Asn Ala Thr
210 215 220

Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Asp Gly Phe
225 230 235 240

Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Pro Ile Glu Asn
245 250 255

Glu Glu Glu Asp Asp Glu Lys His Ile Phe Ser Asp Asp Ser Ser Glu
260 265 270

Leu Thr Ile Arg Asn Val Asp Lys Asn Asp Glu Ala Glu Tyr Val Cys
275 280 285

Ile Ala Glu Asn Lys Ala Gly Glu Gln Asp Ala Ser Ile His Leu Lys
290 295 300

Val Phe Ala Lys Pro Lys Ile Thr Tyr Val Glu Asn Gln Thr Ala Met
305 310 315 320

Glu Leu Glu Glu Gln Val Thr Leu Thr Cys Glu Ala Ser Gly Asp Pro
325 330 335

Ile Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu
340 345 350

Glu Lys Ala Ser Trp Thr Arg Pro Glu Lys Gln Glu Thr Leu Asp Gly
355 360 365

His Met Val Val Arg Ser His Ala Arg Val Ser Ser Leu Thr Leu Lys
370 375 380

Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile Cys Thr Ala Ser Asn
385 390 395 400

Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu Glu Val Gln Tyr Ala
405 410 415

Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr Trp Glu Gly Asn Gln
420 425 430

Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro Ser Ala Thr Ile Ser
435 440 445

Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser Asn Tyr Ser Asn Ile
450 455 460

Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu Glu Val Thr Pro Asp
465 470 475 480

Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr Ala Val Asn Arg Ile
485 490 495

Gly Gln Glu Ser Leu Glu Phe Ile Leu Val Gln Ala Asp Thr Pro Ser
500 505 510

Ser Pro Ser Ile Asp Arg Val Glu Pro Tyr Ser Ser Thr Ala Gln Val
515 520 525

Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val Pro Ile Leu Lys Tyr
530 535 540

Lys Ala Glu Trp Lys Ser Leu Gly Glu Glu Ala Trp His Ser Lys Trp
545 550 555 560

Tyr Asp Ala Lys Glu Ala Asn Met Glu Gly Ile Val Thr Ile Met Gly
565 570 575

Leu Lys Pro Glu Thr Arg Tyr Ala Val Arg Leu Ala Ala Leu Asn Gly
580 585 590

Lys Gly Leu Gly Glu Ile Ser Ala Ala Thr Glu Phe Lys Thr Gln Pro
595 600 605

Val Arg Glu Pro Ser Ala Pro Lys Leu Glu Gly Gln Met Gly Glu Asp
610 615 620

Gly Asn Ser Ile Lys Val Asn Leu Ile Lys Gln Asp Asp Gly Gly Ser
625 630 635 640

Pro Ile Arg His Tyr Leu Val Lys Tyr Arg Ala Leu Ala Ser Glu Trp
645 650 655

Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser Asp His Val Met Leu Lys
660 665 670

Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val Tyr Val Val Ala Glu Asn
675 680 685

Gln Gln Gly Lys Ser Lys Ala Ala His Phe Val Phe Arg Thr Ser Ala
690 695 700

Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser Pro Thr Ala Gly Leu Ser
705 710 715 720

Thr Gly Ala Ile Val Gly Ile Leu Ile Val Ile Phe Val Leu Leu Leu
725 730 735

Val Val Met Asp Ile Thr Cys Tyr Phe Leu Asn Lys Cys Gly Leu Leu
740 745 750

Met Cys Ile Ala Val Asn Leu Cys Gly Lys Ala Gly Pro Gly Ala Lys
755 760 765

Gly Lys Asp Met Glu Glu Gly Lys Ala Ala Phe Ser Lys Asp Glu Ser
770 775 780

Lys Glu Pro Ile Val Glu Val Arg Thr Glu Glu Glu Arg Thr Pro Asn
785 790 795 800

His Asp Gly Gly Lys His Thr Glu Pro Asn Glu Thr Thr Pro Leu Thr
805 810 815

Glu Pro Glu Lys Gly Pro Val Glu Thr Lys Ser Glu Pro Gln Glu Ser
820 825 830

Glu Ala Lys Pro Ala Pro Thr Glu Val Lys Thr Val Pro Asn Glu Ala
835 840 845

Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala
850 855

<210> 45

<211> 848

<212> PRT

<213> Homo sapiens

<400> 45

Met Leu Gln Thr Lys Asp Leu Ile Trp Thr Leu Phe Phe Leu Gly Thr

1

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15

Ala Val Ser Leu Gln Val Asp Ile Val Pro Ser Gln Gly Glu Ile Ser
20 25 30

Val Gly Glu Ser Lys Phe Phe Leu Cys Gln Val Ala Gly Asp Ala Lys
35 40 45

Asp Lys Asp Ile Ser Trp Phe Ser Pro Asn Gly Glu Lys Leu Thr Pro
50 55 60

Asn Gln Gln Arg Ile Ser Val Val Trp Asn Asp Asp Ser Ser Ser Thr
65 70 75 80

Leu Thr Ile Tyr Asn Ala Asn Ile Asp Asp Ala Gly Ile Tyr Lys Cys
85 90 95

Val Val Thr Gly Glu Asp Gly Ser Glu Ser Glu Ala Thr Val Asn Val
100 105 110

Lys Ile Phe Gln Lys Leu Met Phe Lys Asn Ala Pro Thr Pro Gln Glu
115 120 125

Phe Arg Glu Gly Glu Asp Ala Val Ile Val Cys Asp Val Val Ser Ser
130 135 140

Leu Pro Pro Thr Ile Ile Trp Lys His Lys Gly Arg Asp Val Ile Leu
145 150 155 160

Lys Lys Asp Val Arg Phe Ile Val Leu Ser Asn Asn Tyr Leu Gln Ile
165 170 175

Arg Gly Ile Lys Lys Thr Asp Glu Gly Thr Tyr Arg Cys Glu Gly Arg
180 185 190

Ile Leu Ala Arg Gly Glu Ile Asn Phe Lys Asp Ile Gln Val Ile Val
195 200 205

Asn Val Pro Pro Thr Ile Gln Ala Arg Gln Asn Ile Val Asn Ala Thr
210 215 220

Ala Asn Leu Gly Gln Ser Val Thr Leu Val Cys Asp Ala Glu Gly Phe
225 230 235 240

Pro Glu Pro Thr Met Ser Trp Thr Lys Asp Gly Glu Gln Ile Glu Gln
245 250 255

Glu Glu Asp Asp Glu Lys Tyr Ile Phe Ser Asp Asp Ser Ser Gln Leu
260 265 270

Thr Ile Lys Lys Val Asp Lys Asn Asp Glu Ala Glu Tyr Ile Cys Ile
275 280 285

Ala Glu Asn Lys Ala Gly Glu Gln Asp Ala Thr Ile His Leu Lys Val
290 295 300

Phe Ala Lys Pro Lys Ile Thr Tyr Val Glu Asn Gln Thr Ala Met Glu
305 310 315 320

Leu Glu Glu Gln Val Thr Leu Thr Cys Glu Ala Ser Gly Asp Pro Ile
325 330 335

Pro Ser Ile Thr Trp Arg Thr Ser Thr Arg Asn Ile Ser Ser Glu Glu
340 345 350

Lys Thr Leu Asp Gly His Met Val Val Arg Ser His Ala Arg Val Ser
355 360 365

Ser Leu Thr Leu Lys Ser Ile Gln Tyr Thr Asp Ala Gly Glu Tyr Ile
370 375 380

Cys Thr Ala Ser Asn Thr Ile Gly Gln Asp Ser Gln Ser Met Tyr Leu
385 390 395 400

Glu Val Gln Tyr Ala Pro Lys Leu Gln Gly Pro Val Ala Val Tyr Thr
405 410 415

Trp Glu Gly Asn Gln Val Asn Ile Thr Cys Glu Val Phe Ala Tyr Pro
420 425 430

Ser Ala Thr Ile Ser Trp Phe Arg Asp Gly Gln Leu Leu Pro Ser Ser
435 440 445

Asn Tyr Ser Asn Ile Lys Ile Tyr Asn Thr Pro Ser Ala Ser Tyr Leu
450 455 460

Glu Val Thr Pro Asp Ser Glu Asn Asp Phe Gly Asn Tyr Asn Cys Thr
465 470 475 480

Ala Val Asn Arg Ile Gly Gln Glu Ser Leu Glu Phe Ile Leu Val Gln
485 490 495

Ala Asp Thr Pro Ser Ser Pro Ser Ile Asp Gln Val Glu Pro Tyr Ser
500 505 510

Ser Thr Ala Gln Val Gln Phe Asp Glu Pro Glu Ala Thr Gly Gly Val
515 520 525

Pro Ile Leu Lys Tyr Lys Ala Glu Trp Arg Ala Val Gly Glu Glu Val
530 535 540

Trp His Ser Lys Trp Tyr Asp Ala Lys Glu Ala Ser Met Glu Gly Ile
545 550 555 560

Val Thr Ile Val Gly Leu Lys Pro Glu Thr Thr Tyr Ala Val Arg Leu
565 570 575

Ala Ala Leu Asn Gly Lys Gly Leu Gly Glu Ile Ser Ala Ala Ser Glu
580 585 590

Phe Lys Thr Gln Pro Val Gln Gly Glu Pro Ser Ala Pro Lys Leu Glu
595 600 605

Gly Gln Met Gly Glu Asp Gly Asn Ser Ile Lys Val Asn Leu Ile Lys
610 615 620

Gln Asp Asp Gly Gly Ser Pro Ile Arg His Tyr Leu Val Arg Tyr Arg
625 630 635 640

Ala Leu Ser Ser Glu Trp Lys Pro Glu Ile Arg Leu Pro Ser Gly Ser
645 650 655

Asp His Val Met Leu Lys Ser Leu Asp Trp Asn Ala Glu Tyr Glu Val
660 665 670

Tyr Val Val Ala Glu Asn Gln Gln Gly Lys Ser Lys Ala Ala His Phe
675 680 685

Val Phe Arg Thr Ser Ala Gln Pro Thr Ala Ile Pro Ala Asn Gly Ser
690 695 700

Pro Thr Ser Gly Leu Ser Thr Gly Ala Ile Val Gly Ile Leu Ile Val
705 710 715 720

Ile Phe Val Leu Leu Leu Val Val Val Asp Ile Thr Cys Tyr Phe Leu
725 730 735

Asn Lys Cys Gly Leu Phe Met Cys Ile Ala Val Asn Leu Cys Gly Lys
740 745 750

Ala Gly Pro Gly Ala Lys Gly Lys Asp Met Glu Glu Gly Lys Ala Ala
755 760 765

Phe Ser Lys Asp Glu Ser Lys Glu Pro Ile Val Glu Val Arg Thr Glu
770 775 780

Glu Glu Arg Thr Pro Asn His Asp Gly Gly Lys His Thr Glu Pro Asn
785 790 795 800

Glu Thr Thr Pro Leu Thr Glu Pro Glu Lys Gly Pro Val Glu Ala Lys
805 810 815

Pro Glu Cys Gln Glu Thr Glu Thr Lys Pro Ala Pro Ala Glu Val Lys
820 825 830

Thr Val Pro Asn Asp Ala Thr Gln Thr Lys Glu Asn Glu Ser Lys Ala
835 840 845